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Sequence Listing could not be accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2010; month=2; day=10; hr=18; min=0; sec=56; ms=862;]

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Reviewer Comments:

<210> 6

<211> 1310

<212> PRT

<213> Varicella zoster

<220>

<221> misc_feature

<222> (99)..(99)

<223> The 'Xaa' at location 99 stands for Thr, or Met.

<220>

<221> misc_feature

<222> (512)..(512)

<223> The 'Xaa' at location 512 stands for Ala, or Val.

<220>

<221> misc_feature

<222> (1275)..(1275)

<223> The 'Xaa' at location 1275 stands for Ser, Leu, or Xaa.

The above <223> response describing the "Xaa" at location 1275 contains an error: "Xaa" cannot represent an "Xaa". "The 'Xaa' at location 1275 stands for Ser or Leu" would be correct.

Application No: 10591787 Version No: 3.0

Input Set:

Output Set:

Started: 2010-01-28 17:10:23.171
Finished: 2010-01-28 17:10:35.201
Elapsed: 0 hr(s) 0 min(s) 12 sec(s) 30 ms
Total Warnings: 5
Total Errors: 0
No. of SeqIDs Defined: 91
Actual SeqID Count: 91

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)

SEQUENCE LISTING

<110> Nagaike, Kazuhiro
Mori, Yasuko
Gomi, Yasuyuki
Takahashi, Michiaki
Kouichi, Yamanishi

<120> Recombinant varicella-zoster virus

<130> 59150-8037

<140> 10591787

<141> 2010-01-28

<150> PCT/JP2005/003652

<151> 2005-03-05

<150> JP 2004-063277

<151> 2004-03-05

<160> 91

<170> PatentIn version 3.2

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<222> (99)..(99)

<223> The 'Xaa' at location 99 stands for Thr, or Met.

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<222> (512)..(512)

<223> The 'Xaa' at location 512 stands for Ala, or Val.

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<222> (1275)..(1275)

<223> The 'Xaa' at location 1275 stands for Ser, or Leu.

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acacgtttta agtactgttg gaactccctc accaaccgca aycgcaatcc tttgaagget 180

gcgagagcgt ttggaaaact cgggtacgtc taaattcacc ccagygcg atg gat acg 237

Met Asp Thr

1

ccg ccg atg cag cgc tct aca ccc caa cgc gcg ggg tcg cct gat act 285

Pro Pro Met Gln Arg Ser Thr Pro Gln Arg Ala Gly Ser Pro Asp Thr

5

10

15

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Leu	Glu	Leu	Met	Asp	Leu	Leu	Asp	Ala	Ala	Ala	Ala	Ala	Ala	Glu	His	
20					25					30					35	
agg	gcc	cgg	gtg	gtc	acc	tcg	agt	cag	cct	gac	gat	cta	cta	ttt	gga	381
Arg	Ala	Arg	Val	Val	Thr	Ser	Ser	Gln	Pro	Asp	Asp	Leu	Leu	Phe	Gly	
			40					45						50		
gag	aac	ggg	gtc	atg	gtg	gga	cgg	gaa	cat	gag	atc	gtt	tca	att	ccc	429
Glu	Asn	Gly	Val	Met	Val	Gly	Arg	Glu	His	Glu	Ile	Val	Ser	Ile	Pro	
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gag	cta	aca	caa	gac	gac	tac	gta	tgc	gag	gac	ggc	cag	gat	cta	ayg	525
Glu	Leu	Thr	Gln	Asp	Asp	Tyr	Val	Cys	Glu	Asp	Gly	Gln	Asp	Leu	Xaa	
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ggc	tcg	cct	gta	atc	ccg	ctg	gcc	gag	gtc	ttc	cac	acc	cga	ttc	tcg	573
Gly	Ser	Pro	Val	Ile	Pro	Leu	Ala	Glu	Val	Phe	His	Thr	Arg	Phe	Ser	
100					105					110					115	
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Glu	Ala	Gly	Ala	Arg	Glu	Pro	Thr	Gly	Ala	Asp	Arg	Ser	Leu	Glu	Thr	
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gtc	tct	ctc	gga	acg	aag	ctt	gct	agg	tct	cca	aaa	cca	ccg	atg	aac	669
Val	Ser	Leu	Gly	Thr	Lys	Leu	Ala	Arg	Ser	Pro	Lys	Pro	Pro	Met	Asn	
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Asp	Gly	Glu	Thr	Gly	Arg	Gly	Thr	Thr	Pro	Pro	Phe	Pro	Gln	Ala	Phe	
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Ser	Pro	Val	Ser	Pro	Ala	Ser	Pro	Val	Gly	Asp	Ala	Ala	Gly	Asn	Asp	
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caa	cgg	gaa	gac	cag	cgg	tct	ata	ccc	cga	caa	acg	acg	aga	gga	aat	813
Gln	Arg	Glu	Asp	Gln	Arg	Ser	Ile	Pro	Arg	Gln	Thr	Thr	Arg	Gly	Asn	
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Ser	Pro	Gly	Leu	Pro	Ser	Val	Val	His	Arg	Asp	Arg	Gln	Thr	Gln	Ser	
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atc	tcg	ggc	aaa	aag	ccg	ggc	gat	gag	caa	gcg	ggc	cat	gcg	cat	gca	909
Ile	Ser	Gly	Lys	Lys	Pro	Gly	Asp	Glu	Gln	Ala	Gly	His	Ala	His	Ala	
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Ser	Gly	Asp	Gly	Val												

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Lys Ser Pro Lys Lys Lys Thr Leu Lys Val Lys Val Pro Leu Pro Ala	
245 250 255	
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Arg Lys Pro Gly Gly Pro Val Pro Gly Pro Val Glu Gln Leu Tyr His	
260 265 270 275	
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Val Leu Ser Asp Ser Val Pro Ala Lys Gly Ala Lys Ala Asp Leu Pro	
280 285 290	
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Phe Glu Thr Asp Asp Thr Arg Pro Arg Lys His Asp Ala Arg Gly Ile	
295 300 305	
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Thr Pro Arg Val Pro Gly Arg Ser Ser Gly Gly Lys Pro Arg Ala Phe	
310 315 320	
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Leu Ala Leu Pro Gly Arg Ser His Ala Pro Asp Pro Ile Glu Asp Asp	
325 330 335	
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Ser Pro Val Glu Lys Lys Pro Lys Ser Arg Glu Phe Val Ser Ser Ser	
340 345 350 355	
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Ser Ser Ser Ser Ser Trp Gly Ser Ser Ser Glu Asp Glu Asp Asp Glu	
360 365 370	
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Pro Arg Arg Val Ser Val Gly Ser Glu Thr Thr Gly Ser Arg Ser Gly	
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Arg Glu His Ala Pro Ser Pro Ser Asn Ser Asp Asp Ser Asp Ser Asn	
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Asp Gly Gly Ser Thr Lys Gln Asn Ile Gln Pro Gly Tyr Arg Ser Ile	
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Pro Gly Arg Gln Arg Gln Lys Ser Phe Ser Leu Pro Arg Ser Arg Thr	
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Pro Ile Ile Pro Pro Val Ser Gly Pro Leu Met Met Pro Asp Gly Ser	
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Pro Trp Pro Gly Ser Ala Pro Leu Pro Ser Asn Arg Val Arg Phe Gly	
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Pro Ser Gly Glu Thr Arg Glu Gly His Trp Glu Asp Glu Ala Val Arg	
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Ala Ala Arg Ala Arg Tyr Glu Ala Ser Thr Glu Pro Xaa Pro Leu Tyr	
500 505 510 515	
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Val Pro Glu Leu Gly Asp Pro Ala Arg Gln Tyr Arg Ala Leu Ile Asn	
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Leu Ile Tyr Cys Pro Asp Arg Asp Pro Ile Ala Trp Leu Gln Asn Pro	
535 540 545	
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565 570 575	
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Pro Val Pro His Val Gly Glu Ala Met Ala Thr Gly Glu Ala Leu Trp	
580 585 590 595	
gct ctc ccc cac gcg gcc gcg gcc gtg gct atg agc cgt cgg tac gac	2061
Ala Leu Pro His Ala Ala Ala Val Ala Met Ser Arg Arg Tyr Asp	
600 605 610	
cgg gcc caa aaa cac ttt atc cta cag agt ctc cgc aga gcc ttt gcc	2109
Arg Ala Gln Lys His Phe Ile Leu Gln Ser Leu Arg Arg Ala Phe Ala	
615 620 625	
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Gly Met Ala Tyr Pro Glu Ala Thr Gly Ser Ser Pro Ala Ala Arg Ile	
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Ser Arg Gly His Pro Ser Pro Thr Thr Pro Ala Thr Gln Thr Pro Asp	
645 650 655	
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Pro Gln Pro Ser Ala Ala Ala Arg Ser Leu Ser Val Cys Pro Pro Asp	
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Asp Arg Leu Arg Thr Pro Arg Lys Arg Lys Ser Gln Pro Val Glu Ser	
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Arg Ser Leu Leu Asp Lys Ile Arg Glu Thr Pro Val Ala Asp Ala Arg	

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Val Ala Asp Asp His Val Val Ser Lys Ala Lys Arg Arg Val Ser Glu			
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Pro Val Thr Ile Thr Ser Gly Pro Val Val Asp Pro Pro Ala Val Ile			
725	730	735	
acg atg cca ctt gac gga ccg gcc cca aac ggg gga ttt cgg cgt att			2493
Thr Met Pro Leu Asp Gly Pro Ala Pro Asn Gly Gly Phe Arg Arg Ile			
740	745	750	755
ccc cgg ggg gcc ctg cat acc ccg gtc ccg tcg gac cag gct cgc aag			2541
Pro Arg Gly Ala Leu His Thr Pro Val Pro Ser Asp Gln Ala Arg Lys			
760	765	770	
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Ala Tyr Cys Thr Pro Glu Thr Ile Ala Arg Leu Val Asp Asp Pro Leu			
775	780	785	
ttt ccc acg gcc tgg cgc cct gcg cta agc ttt gat ccc ggc gcc ttg			2637
Phe Pro Thr Ala Trp Arg Pro Ala Leu Ser Phe Asp Pro Gly Ala Leu			
790	795	800	
gcg gaa atc gcc gct cgg cgt ccg ggc gga gga gac cga cgg ttt ggt			2685
Ala Glu Ile Ala Ala Arg Arg Pro Gly Gly Gly Asp Arg Arg Phe Gly			
805	810	815	
cca ccc agc gga gtg gag gcg ctg cga cgg agg tgc gcc tgg atg cgg			2733
Pro Pro Ser Gly Val Glu Ala Leu Arg Arg Arg Cys Ala Trp Met Arg			
820	825	830	835
cag atc cca gac ccg gag gat gtg agg ctt ctg atc atc tac gat ccg			2781
Gln Ile Pro Asp Pro Glu Asp Val Arg Leu Leu Ile Ile Tyr Asp Pro			
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Leu Pro Gly Glu Asp Ile Asn Gly Pro Leu Glu Ser Thr Leu Ala Thr			
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Asp Pro Gly Pro Ser Trp Ser Pro Ser Arg Gly Gly Leu Ser Val Val			
870	875	880	
ctg gca gcc ctg agt aac cgg ttg tgc ctg ccg agc act cat gcc tgg			2925
Leu Ala Ala Leu Ser Asn Arg Leu Cys Leu Pro Ser Thr His Ala Trp			
885	890	895	
gcc ggg aac tgg acc ggc ccg ccg gac gtg tcc gct ttg aac gcc cgg			2973
Ala Gly Asn Trp Thr Gly Pro Pro Asp Val Ser Ala Leu Asn Ala Arg			
900	905	910	915
ggc gtt tta tta ctg tcg acc cga gac ctg gcc ttt gcc ggg gcc gtc			3021
Gly Val Leu Leu Leu Ser Thr Arg Asp Leu Ala Phe Ala Gly Ala Val			
920	925	930	

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950 955 960	
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Ser Gln Tyr His Val Tyr Val Arg Ala Pro Ala Arg Pro Asp Ala Gln	
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Ala Val Val Arg Trp Pro Asp Ser Ala Val Thr Glu Gly Leu Ala Arg	
980 985 990 995	
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Ala Val Phe Ala Ser Ser Arg Thr Phe Gly Pro Ala Ser Phe Ala	
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Arg Ile Glu Thr Ala Phe Ala Asn Leu Tyr Pro Gly Glu Gln Pro	
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Glu Asp Ala Trp Asp	Ser Glu Glu Gly Gly	Gly Asp Asp Gly Asp	
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Ala Pro Gly Ser Ser	Phe Gly Val Ser Val	Val Ser Val Al	